

#5

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/325,019

DATE: 06/15/1999
TIME: 18:07:54

Input Set: I325019.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

see P. 5

ENTERED

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1  <110> APPLICANT: Young, Paul
2      Ruben, Steven M.
3  <120> TITLE OF INVENTION: Connective Tissue Growth Factor-4
4  <130> FILE REFERENCE: PF467
5  <140> CURRENT APPLICATION NUMBER: US/09/325,019
6  <141> CURRENT FILING DATE: 1999-06-03
7  <150> EARLIER APPLICATION NUMBER: 60/088,320
8  <151> EARLIER FILING DATE: 1998-06-05
9  <160> NUMBER OF SEQ ID NOS: 27
10 <170> SOFTWARE: PatentIn Ver. 2.0
11 <210> SEQ ID NO 1
12 <211> LENGTH: 3658
13 <212> TYPE: DNA
14 <213> ORGANISM: Homo sapiens
15 <220> FEATURE:
16 <221> NAME/KEY: CDS
17 <222> LOCATION: (3)..(1007)
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20      Asp Phe Thr Pro Ala Pro Leu Glu Asp Thr Ser Ser Arg Pro Gln
21      1              5              10              15
22      ttc tgc aag tgg cca tgt gag tgc ccg cca tcc cca ccc cgc tgc ccg      95
23      Phe Cys Lys Trp Pro Cys Glu Cys Pro Pro Ser Pro Pro Arg Cys Pro
24      20              25              30
25      ctg ggg gtc agc ctc atc aca gat ggc tgt gag tgc tgt aag atg tgc      143
26      Leu Gly Val Ser Leu Ile Thr Asp Gly Cys Glu Cys Cys Lys Met Cys
27      35              40              45
28      gct cag cag ctt ggg gac aac tgc acg gag gct gcc atc tgt gac ccc      191
29      Ala Gln Gln Leu Gly Asp Asn Cys Thr Glu Ala Ala Ile Cys Asp Pro
30      50              55              60
31      cac cgg ggc ctc tac tgt gac tac agc ggg gac cgc ccg agg tac gca      239
32      His Arg Gly Leu Tyr Cys Asp Tyr Ser Gly Asp Arg Pro Arg Tyr Ala
33      65              70              75
34      ata gga gtg tgt gca cag gtg gtc ggt gtg ggc tgc gtc ctg gat ggg      287
35      Ile Gly Val Cys Ala Gln Val Val Gly Val Gly Cys Val Leu Asp Gly
36      80              85              90              95
37      gtg cgc tac aac aac ggc cag tcc ttc cag cct aac tgc aag tac aac      335
38      Val Arg Tyr Asn Asn Gly Gln Ser Phe Gln Pro Asn Cys Lys Tyr Asn
39      100              105              110
40      tgc acg tgc atc gac ggc gcg gtg ggc tgc aca cca ctg tgc ctc cga      383
41      Cys Thr Cys Ile Asp Gly Ala Val Gly Cys Thr Pro Leu Cys Leu Arg
42      115              120              125
43      gtg cgc ccc ccg cgt ctc tgg tgc ccc cac ccg cgg cgc gtg agc ata      431
44      Val Arg Pro Pro Arg Leu Trp Cys Pro His Pro Arg Arg Val Ser Ile

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95   cagctgctga ctggcagggc tttgggcagt tggccaggct cttccttgaa tcttctccct 1847
96   tgtcctgctt ggggttcata ggaattggta aggcctctgg actggcctgt ctggcccctg 1907
97   agagtgggtg cctggaacac tcctctactc ttacagagcc ttgagagacc cagctgcaga 1967
98   ccatgccaga ccactgaaa tgaccaagac aggttcaggt aggggtgtgg gtcaaaccaa 2027
99   gaagtgggtg cccttggtag cagcctgggg tgacctctag agctggaggc tgtgggactc 2087
100  caggggcccc cgtgttcagg acacatctat tgcagagact catttcacag cctttcgttc 2147
101  tgctgaccaa atggccagtt ttctggtagg aagatggagg tttaccagtt gtttagaaac 2207
102  agaaatagac ttaataaagg tttaaagctg aagaggttga agctaaaagg aaaaggttgt 2267
103  tgtaaatgaa tatcaggcta ttatttattg tattaggaat atataatatt tactgttaga 2327
104  attcttttat ttagggcctt ttctgtgcca gacattgctc tcagtgtctt gcatgtatta 2387
105  gctcactgaa tcttcacgac aatgttgaga agttcccatt attatttctg ttcttacaaa 2447
106  tgtgaaacgg aagctcatag aggtgagaaa actcaaccag agtcaccagc ttggtgactg 2507
107  ggaaagttag gattcagatc gaaattggac tgtctttata acccatattt tccccctgtt 2567
108  tttagagctt ccaaagtgtg cagaatagga aaacattgca ataaatggct tgatttttta 2627
109  atgtcatttt tccctcttat agtctttcta gctccttttc aaaagacgag aatatctgat 2687
110  tttctgataa tttagggtgct taagcatcca aaatacatgg gacacacaaa aatccaggaa 2747
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112  tgattctgtt tacccaatgc tgcataattg atgttgtgta gttattcaca gggaattctg 2867
113  tgcagtgtgc agagagattc ctaaacggga aaaggactgg gaatacatcc tccttactgt 2927
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115  aatacaggaa gctgtgcatg tgttcctact tttattcgaa gctctcttct tccaagcta 3047
116  catgaaaata gaattttaac agtcaaaatt ttatattaag tgtcttagca aaagagacat 3107
117  ttaatatctt aaagaaatgc atatgtatgt atacatatat ttgtgtatgc gtatgcaaga 3167
118  attcttgtat aaagagaatt cactccatga atgatctctt ctgtaagtca gtgtgaatca 3227
119  tgttagattt tctgagagtg aaaacacctg ccatctacaa attacaaggc tggataacag 3287
120  ctactcccat ttgaaattca gtggaaaccc aagagctagg ttcttactga atttgcattc 3347
121  caatttggga aactgaactt agctttcaaa gatcatagga agtctgggtg gagaaactag 3407
122  ggattattct ggcaatgggt ggaggaagggt ggtcagaata acccagtcgc cattggtttt 3467
123  gagaaacgga actatcttat gcagagcccc gagggcaagt ctcaaaccga tgggttgaag 3527
124  ccatggagaa ggaaatttgg atccaatgta atgaagctct ttctaagtca gaatttcctc 3587
125  gcaatggtgt ggcttgattc aataaaaatt aagaataata aatataatgg aaaaaaaaaa 3647
126  aaaaaaaaaa a                                     3658

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127 <210> SEQ ID NO 2

128 <211> LENGTH: 335

129 <212> TYPE: PRT

130 <213> ORGANISM: Homo sapiens

131 <400> SEQUENCE: 2

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134   Cys Lys Trp Pro Cys Glu Cys Pro Pro Ser Pro Pro Arg Cys Pro Leu
135             20             25             30
136   Gly Val Ser Leu Ile Thr Asp Gly Cys Glu Cys Cys Lys Met Cys Ala
137             35             40             45
138   Gln Gln Leu Gly Asp Asn Cys Thr Glu Ala Ala Ile Cys Asp Pro His
139             50             55             60
140   Arg Gly Leu Tyr Cys Asp Tyr Ser Gly Asp Arg Pro Arg Tyr Ala Ile
141             65             70             75             80
142   Gly Val Cys Ala Gln Val Val Gly Val Gly Cys Val Leu Asp Gly Val
143             85             90             95
144   Arg Tyr Asn Asn Gly Gln Ser Phe Gln Pro Asn Cys Lys Tyr Asn Cys

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145          100          105          110
146 Thr Cys Ile Asp Gly Ala Val Gly Cys Thr Pro Leu Cys Leu Arg Val
147          115          120          125
148 Arg Pro Pro Arg Leu Trp Cys Pro His Pro Arg Arg Val Ser Ile Pro
149          130          135          140
150 Gly His Cys Cys Glu Gln Trp Val Cys Glu Asp Asp Ala Lys Arg Pro
151          145          150          155          160
152 Arg Lys Thr Ala Pro Arg Asp Thr Gly Ala Phe Asp Ala Val Gly Glu
153          165          170          175
154 Val Glu Ala Trp His Arg Asn Cys Ile Ala Tyr Thr Ser Pro Trp Ser
155          180          185          190
156 Pro Cys Ser Thr Ser Cys Gly Leu Gly Val Ser Thr Arg Ile Ser Asn
157          195          200          205
158 Val Asn Ala Gln Cys Trp Pro Glu Gln Glu Ser Arg Leu Cys Asn Leu
159          210          215          220
160 Arg Pro Cys Asp Val Asp Ile His Thr Leu Ile Lys Ala Gly Lys Lys
161          225          230          235          240
162 Cys Leu Ala Val Tyr Gln Pro Glu Ala Ser Met Asn Phe Thr Leu Ala
163          245          250          255
164 Gly Cys Ile Ser Thr Arg Ser Tyr Gln Pro Lys Tyr Cys Gly Val Cys
165          260          265          270
166 Met Asp Asn Arg Cys Cys Ile Pro Tyr Lys Ser Lys Thr Ile Asp Val
167          275          280          285
168 Ser Phe Gln Cys Pro Asp Gly Leu Gly Phe Ser Arg Gln Val Leu Trp
169          290          295          300
170 Ile Asn Ala Cys Phe Cys Asn Leu Ser Cys Arg Asn Pro Asn Asp Ile
171          305          310          315          320
172 Phe Ala Asp Leu Glu Ser Tyr Pro Asp Phe Ser Glu Ile Ala Asn
173          325          330          335
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175 <211> LENGTH: 367
176 <212> TYPE: PRT
177 <213> ORGANISM: Mus musculus
178 <400> SEQUENCE: 3
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180 1 5 10 15
181 Val Gly Asn Ile Leu Ala Thr Ala Leu Ser Pro Thr Pro Thr Thr Met
182 20 25 30
183 Thr Phe Thr Pro Ala Pro Leu Glu Glu Thr Thr Thr Arg Pro Glu Phe
184 35 40 45
185 Cys Lys Trp Pro Cys Glu Cys Pro Gln Ser Pro Pro Arg Cys Pro Leu
186 50 55 60
187 Gly Val Ser Leu Ile Thr Asp Gly Cys Glu Cys Cys Lys Ile Cys Ala
188 65 70 75 80
189 Gln Gln Leu Gly Asp Asn Cys Thr Glu Ala Ala Ile Cys Asp Pro His
190 85 90 95
191 Arg Gly Leu Tyr Cys Asp Tyr Ser Gly Asp Arg Pro Arg Tyr Ala Ile
192 100 105 110
193 Gly Val Cys Ala Gln Val Val Gly Val Gly Cys Val Leu Asp Gly Val
194 115 120 125

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195   Arg Tyr Thr Asn Gly Glu Ser Phe Gln Pro Asn Cys Arg Tyr Asn Cys
196       130                      135                      140
197   Thr Cys Ile Asp Gly Thr Val Gly Cys Thr Pro Leu Cys Leu Ser Pro
198   145                      150                      155                      160
199   Arg Pro Pro Arg Leu Trp Cys Arg Gln Pro Arg His Val Arg Val Pro
200                      165                      170                      175
201   Gly Gln Cys Cys Glu Gln Trp Val Cys Asp Asp Ala Arg Arg Pro
202                      180                      185                      190
203   Arg Gln Thr Ala Leu Leu Asp Thr Arg Ala Phe Ala Ala Ser Gly Ala
204       195                      200                      205
205   Val Glu Gln Arg Tyr Glu Asn Cys Ile Ala Tyr Thr Ser Pro Trp Ser
206   210                      215                      220
207   Pro Cys Ser Thr Thr Cys Gly Leu Gly Ile Ser Thr Arg Ile Ser Asn
208   225                      230                      235                      240
209   Val Asn Ala Arg Cys Trp Pro Glu Gln Glu Ser Arg Leu Cys Asn Leu
210                      245                      250                      255
211   Arg Pro Cys Asp Val Asp Ile Gln Leu His Ile Lys Ala Gly Lys Lys
212       260                      265                      270
213   Cys Leu Ala Val Tyr Gln Pro Glu Glu Ala Thr Asn Phe Thr Leu Ala
214       275                      280                      285
215   Gly Cys Val Ser Thr Arg Thr Tyr Arg Pro Lys Tyr Cys Gly Val Cys
216   290                      295                      300
217   Thr Asp Asn Arg Cys Cys Ile Pro Tyr Lys Ser Lys Thr Ile Ser Val
218   305                      310                      315                      320
219   Asp Phe Gln Cys Pro Glu Gly Pro Gly Phe Ser Arg Gln Val Leu Trp
220                      325                      330                      335
221   Ile Asn Ala Cys Phe Cys Asn Leu Ser Cys Arg Asn Pro Asn Asp Ile
222       340                      345                      350
223   Phe Ala Asp Leu Glu Ser Tyr Pro Asp Phe Glu Glu Ile Ala Asn
224       355                      360                      365
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226 <211> LENGTH: 349
227 <212> TYPE: PRT
228 <213> ORGANISM: Homo sapiens
229 <400> SEQUENCE: 4
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232   Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro
233       20                      25                      30
234   Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
235       35                      40                      45
236   Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
237       50                      55                      60
238   Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
239       65                      70                      75                      80
240   Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
241       85                      90                      95
242   Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
243       100                     105                     110
244   Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I325019.RAW

Line	? Error/Warning	Original Text
445	W "N" or "Xaa" used: Feature required	tccatggctt caacccatgg gtctgagact tgccttcc
448	W "N" or "Xaa" used: Feature required	aattggagat gcaattcnag taagaacctta gccctnng
449	W "N" or "Xaa" used: Feature required	agtgagccgt tatccagcct gnaaattngt aaanggca
450	W "N" or "Xaa" used: Feature required	tncaacagga ttcacacggc ttacggaggg gtcctcca
451	W "N" or "Xaa" used: Feature required	atctggcaaa ggnnncnaan tttggaacaa caagcatc
549	W "N" or "Xaa" used: Feature required	ggcanagttt tttttttcca ttatatattat tattctta
551	W "N" or "Xaa" used: Feature required	tccatggctt caacccatgg gtctgagact tgccttcc
554	W "N" or "Xaa" used: Feature required	aattgagatg caattccagt aagaaccaag ccttgggg
555	W "N" or "Xaa" used: Feature required	gngcgttnnc cagcntgnaa ttggnaaagg cagggggt
556	W "N" or "Xaa" used: Feature required	ggttccaccg gcttnacgag gggccntcca gggggaat
557	W "N" or "Xaa" used: Feature required	gancccantt ngtnaaaaaa gncttctgga aaaaagcc
573	W "N" or "Xaa" used: Feature required	caaggtatac agtggtgctc attaaatact tgatgaat
574	W "N" or "Xaa" used: Feature required	ctacttttnt tcgaagctct cttcttccaa agctacat
675	W "N" or "Xaa" used: Feature required	ggcagagtgt atacatatat ttgtgtatgc gtatgaag
676	W "N" or "Xaa" used: Feature required	cactccatga atganctctt ctgtagtnna gtgtgaat
677	W "N" or "Xaa" used: Feature required	aaaaacacct gccatctaca aattnacaag gctggata
678	W "N" or "Xaa" used: Feature required	attcagtggg aaaccaaga gctagggttct tactggaa
680	W "N" or "Xaa" used: Feature required	attattcctg ggcaatgggg tgggaggnag gtgggtnc
681	W "N" or "Xaa" used: Feature required	tggttttgag gaacggnant atcttatggc gngcccng
682	W "N" or "Xaa" used: Feature required	gttnnaggcc tgggggaggg aattttgggt cccatgta
709	W "N" or "Xaa" used: Feature required	ggcacagcgc tcagcagctt ggggacaact gcacggan
712	W "N" or "Xaa" used: Feature required	tnccagccta aactggcaat gacaactgcc acgtgnca
764	W "N" or "Xaa" used: Feature required	Trp Ser Xaa Trp Ser